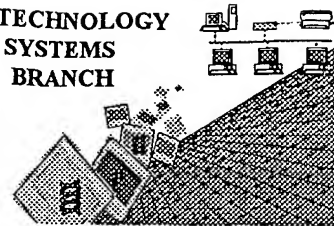


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BIOTECHNOLOGY
SYSTEMS
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RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/619,359
Source: O/PK
Date Processed by STIC: 7/28/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
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Revised 04/24/2003



OIKE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/619,359

DATE: 07/28/2003

TIME: 08:59:07

Input Set : A:\G00307-70020.txt

Output Set: N:\CRF4\07282003\J619359.raw

4 <110> APPLICANT: STOCKER, PENNY J.
 5 STEIMEL-CRESPI, DOROTHY T.
 6 CRESPI, CHARLES L.
 9 <120> TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
 12 <130> FILE REFERENCE: G00307.70020.US
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/619,359
 C--> 14 <141> CURRENT FILING DATE: 2003-07-14
 14 <150> PRIOR APPLICATION NUMBER: US 60/156,921
 15 <151> PRIOR FILING DATE: 1999-09-28
 17 <150> PRIOR APPLICATION NUMBER: US 60/158,818
 18 <151> PRIOR FILING DATE: 1999-10-12
 20 <150> PRIOR APPLICATION NUMBER: US 09/672,810
 21 <151> PRIOR FILING DATE: 2000-09-28
 23 <160> NUMBER OF SEQ ID NOS: 18
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 4186
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Macaca fascicularis
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (100)...(3940)
 36 <400> SEQUENCE: 1

pp 5-6

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38	tcacgacttg gtggccgttc caaggagcgc gaggtcggg atg gat ctt gaa ggg	114
39		
40	Met Asp Leu Glu Gly	
	1 5	
42	gac cgc aat gga gga gca gag aag aag aac ttt ttt aaa ctg aac aat	162
43	Asp Arg Asn Gly Gly Ala Glu Lys Lys Asn Phe Phe Lys Leu Asn Asn	
44	10 15 20	
46	aaa agt aaa aaa gat aag aag gaa agg aaa cca act gtc agt gta ttt	210
47	Lys Ser Lys Lys Asp Lys Lys Glu Arg Lys Pro Thr Val Ser Val Phe	
48	25 30 35	
50	tca atg ttt cgc tat tca aat tgg ctt gac aag ttg tat atg gtg gtg	258
51	Ser Met Phe Arg Tyr Ser Asn Trp Leu Asp Lys Leu Tyr Met Val Val	
52	40 45 50	
54	gga act ttg gct gcc atc atc cat gga gct gga ctt cct ctc atg atg	306
55	Gly Thr Leu Ala Ala Ile Ile His Gly Ala Gly Leu Pro Leu Met Met	
56	55 60 65	

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59	Leu	Val	Phe	Gly	Asp	Met	Thr	Asp	Thr	Phe	Ala	Asn	Ala	Gly	Asn	Leu	
60	70					75					80					85	
62	gga	gat	tta	gga	gct	ctg	ttg	act	aat	agc	agt	aat	atc	act	gat	aca	402
63	Gly	Asp	Leu	Gly	Ala	Leu	Leu	Thr	Asn	Ser	Ser	Asn	Ile	Thr	Asp	Thr	
64					90					95						100	
66	gtg	ccc	gtc	atg	aat	ctg	gag	gaa	gat	atg	acc	agg	tat	gcc	tat	tat	450
67	Val	Pro	Val	Met	Asn	Leu	Glu	Glu	Asp	Met	Thr	Arg	Tyr	Ala	Tyr	Tyr	
68					105					110						115	
70	tac	agt	gga	att	ggg	gct	ggg	gtg	ctg	gtt	gct	gct	tac	att	cag	gtt	498
71	Tyr	Ser	Gly	Ile	Gly	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	Ile	Gln	Val	
72			120					125								130	
74	tca	ttt	tgg	tgc	ctg	gca	gct	gga	aga	caa	ata	cac	aaa	att	aga	aaa	546
75	Ser	Phe	Trp	Cys	Leu	Ala	Ala	Gly	Arg	Gln	Ile	His	Lys	Ile	Arg	Lys	
76			135					140								145	
78	cag	ttt	ttt	cat	gct	ata	atg	cga	cag	gag	ata	ggc	tgg	ttt	gat	gtg	594
79	Gln	Phe	Phe	His	Ala	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	Phe	Asp	Val	
80	150					155					160					165	
82	cac	gat	gtt	ggg	gag	ctt	aac	acc	cgg	ctt	aca	gat	gat	gtc	tcc	aag	642
83	His	Asp	Val	Gly	Glu	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	Val	Ser	Lys	
84					170					175						180	
86	att	aat	gaa	gga	att	ggg	gac	aaa	att	gga	atg	ttc	ttt	cag	tca	atg	690
87	Ile	Asn	Glu	Gly	Ile	Gly	Asp	Lys	Ile	Gly	Met	Phe	Phe	Gln	Ser	Met	
88			185					190								195	
90	gca	aca	ttt	ttc	act	ggg	ttt	ata	gta	gga	ttt	aca	cgt	ggg	tgg	aag	738
91	Ala	Thr	Phe	Phe	Thr	Gly	Phe	Ile	Val	Gly	Phe	Thr	Arg	Gly	Trp	Lys	
92			200					205								210	
94	cta	acc	ctt	gtg	att	ttg	gcc	atc	agt	cct	gtt	ctt	gga	ctg	tca	gct	786
95	Leu	Thr	Leu	Val	Ile	Leu	Ala	Ile	Ser	Pro	Val	Leu	Gly	Leu	Ser	Ala	
96			215					220								225	
98	gca	gtc	tgg	gca	aag	ata	ctg	tct	tca	ttt	act	gat	aaa	gaa	ctc	tta	834
99	Ala	Val	Trp	Ala	Lys	Ile	Leu	Ser	Ser	Phe	Thr	Asp	Lys	Glu	Leu	Leu	
100	230					235					240					245	
102	gct	tat	gca	aaa	gct	gga	gca	gta	gct	gaa	gag	gtc	ttg	gca	gca	att	882
103	Ala	Tyr	Ala	Lys	Ala	Gly	Ala	Val	Ala	Glu	Glu	Val	Leu	Ala	Ala	Ile	
104					250					255						260	
106	aga	act	gtg	att	gca	ttt	gga	gga	caa	aag	aaa	gaa	ctc	gaa	agg	tac	930
107	Arg	Thr	Val	Ile	Ala	Phe	Gly	Gly	Gln	Lys	Lys	Glu	Leu	Glu	Arg	Tyr	
108					265					270						275	
110	aac	aaa	aat	tta	gaa	gaa	gct	aaa	aga	att	ggg	ata	aag	aaa	gct	att	978
111	Asn	Lys	Asn	Leu	Glu	Glu	Ala	Lys	Arg	Ile	Gly	Ile	Lys	Lys	Ala	Ile	
112			280					285								290	
114	aca	gcc	aat	att	tct	ata	ggg	gct	gct	ttc	ctg	ctt	atc	tat	gca	tct	1026
115	Thr	Ala	Asn	Ile	Ser	Ile	Gly	Ala	Ala	Phe	Leu	Leu	Ile	Tyr	Ala	Ser	
116			295					300								305	
118	tat	gct	ctg	gcc	ttc	tgg	tat	ggg	acc	acc	ttg	gtc	ctc	tca	aag	gaa	1074
119	Tyr	Ala	Leu	Ala	Phe	Trp	Tyr	Gly	Thr	Thr	Leu	Val	Leu	Ser	Lys	Glu	
120	310					315					320					325	
122	tat	tct	att	gga	caa	gta	ctc	act	gta	ttc	ttt	tct	gta	tta	att	ggg	1122

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Output Set: N:\CRF4\07282003\J619359.raw

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127	Ala Phe Ser Val Gly Gln Ala Ser Pro Ser Ile Glu Ala Phe Ala Asn	
128		345 350 355
130	gca aga gga gca gct ttt gaa atc ttc aag ata att gat aat aag cca	1218
131	Ala Arg Gly Ala Ala Phe Glu Ile Phe Lys Ile Ile Asp Asn Lys Pro	
132		360 365 370
134	agt att gac agc tat tcg aag agt ggg cac aaa cca gat aat att aag	1266
135	Ser Ile Asp Ser Tyr Ser Lys Ser Gly His Lys Pro Asp Asn Ile Lys	
136		375 380 385
138	gga aat ttg gaa ttc aga aat gtt cac ttc agt tac cca tct cga aaa	1314
139	Gly Asn Leu Glu Phe Arg Asn Val His Phe Ser Tyr Pro Ser Arg Lys	
140		390 395 400 405
142	gaa gtt aag atc ttg aag ggc ctg aac ctg aag gtg cag agt ggg cag	1362
143	Glu Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Gln Ser Gly Gln	
144		410 415 420
146	acg gtg gcc ctg gtt gga aac agc ggc tgt ggg aag agc aca acg gtc	1410
147	Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser Thr Thr Val	
148		425 430 435
150	cag ctg atg cag agg ctt tat gac ccc aca gag ggc atg gtc agt gtt	1458
151	Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr Glu Gly Met Val Ser Val	
152		440 445 450
154	gat gga cag gat att agg acc ata aac gta agg ttt cta cgg gaa atc	1506
155	Asp Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Phe Leu Arg Glu Ile	
156		455 460 465
158	atc ggt gtg gtg agt cag gaa cct gta ttg ttt gcc acc acg ata gct	1554
159	Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala Thr Thr Ile Ala	
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162	gaa aac att cgc tat ggt cgt gaa gat gtc acc atg gat gag att gag	1602
163	Glu Asn Ile Arg Tyr Gly Arg Glu Asp Val Thr Met Asp Glu Ile Glu	
164		490 495 500
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167	Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met Lys Leu Pro	
168		505 510 515
170	cag aaa ttt gac acc ctg gtt gga gag aga ggg gcc cag ctg agt ggt	1698
171	Gln Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln Leu Ser Gly	
172		520 525 530
174	ggg cag aag cag agg atc gcc att gca cgt gcc ctg gtt cgc aac ccc	1746
175	Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala Leu Val Arg Asn Pro	
176		535 540 545
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179	Lys Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser	
180		550 555 560 565
182	gaa gca gtg gtt cag gtg gct ctg gat aag gcc aga aaa ggt cgg acc	1842
183	Glu Ala Val Val Gln Val Ala Leu Asp Lys Ala Arg Lys Gly Arg Thr	
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186	acc att gtg ata gct cat cgt ttg tct acg gtt cgt aat gcc gac gtc	1890
187	Thr Ile Val Ile Ala His Arg Leu Ser Thr Val Arg Asn Ala Asp Val	

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192		600		605		610		
194	gag ctc atg aaa gag aaa ggc att tac ttc aaa ctt gtc aca atg cag							1986
195	Glu Leu Met Lys Glu Lys Gly Ile Tyr Phe Lys Leu Val Thr Met Gln							
196		615		620		625		
198	aca gca gga aat gaa att gaa tta gaa aat gca gct gat gaa tcc aaa							2034
199	Thr Ala Gly Asn Glu Ile Glu Leu Glu Asn Ala Ala Asp Glu Ser Lys							
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202	agt gaa att gat acc ttg gaa atg tct tca cat gat tca gga tcc agt							2082
203	Ser Glu Ile Asp Thr Leu Glu Met Ser Ser His Asp Ser Gly Ser Ser							
204		650		655		660		
206	cta ata aga aaa aga tcc act cgt agg agt gtc cgt gga tca caa ggc							2130
207	Leu Ile Arg Lys Arg Ser Thr Arg Arg Ser Val Arg Gly Ser Gln Gly							
208		665		670		675		
210	caa gac aga aag ctt agt acc aaa gag gct ctg gat gaa agt ata cct							2178
211	Gln Asp Arg Lys Leu Ser Thr Lys Glu Ala Leu Asp Glu Ser Ile Pro							
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214	cca gtt tcc ttt tgg agg att atg aag cta aat tta act gag tgg cct							2226
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216		695		700		705		
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219	Tyr Phe Val Val Gly Val Phe Cys Ala Ile Ile Asn Gly Gly Leu Gln							
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231	Leu Phe Leu Val Leu Gly Ile Val Ser Phe Ile Thr Phe Phe Leu Gln							
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234	ggc ttc aca ttt ggc aaa gct gga gag atc ctc acc aag cgg ctc cga							2466
235	Gly Phe Thr Phe Gly Lys Ala Gly Glu Ile Leu Thr Lys Arg Leu Arg							
236		775		780		785		
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239	Tyr Met Val Phe Arg Ser Met Leu Arg Gln Asp Val Ser Trp Phe Asp							
240	790		795		800		805	
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243	Asp Pro Lys Asn Thr Thr Gly Ala Leu Thr Thr Arg Leu Ala Asn Asp							
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246	gct gct caa gtt aaa ggg gct ata ggt tcc agg ctt gct ata att acc							2610
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248		825		830		835		
250	cag aat ata gca aat ctt ggg aca gga ata att ata tcc tta atc tat							2658
251	Gln Asn Ile Ala Asn Leu Gly Thr Gly Ile Ile Ile Ser Leu Ile Tyr							
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 256 855 860 865
 258 ata gca gga gtt gtt gaa atg aaa atg ttg tct gga caa gca ctg aaa 2754
 259 Ile Ala Gly Val Val Glu Met Lys Met Leu Ser Gly Gln Ala Leu Lys
 260 870 875 880 885
 262 gat aag aaa gaa cta gaa ggt gct ggg aag atc gct act gaa gca ata 2802
 263 Asp Lys Lys Glu Leu Glu Gly Ala Gly Lys Ile Ala Thr Glu Ala Ile
 264 890 895 900
 266 gaa aac ttc cga act gtt gtt tct ttg act cag gag cag aag ttt gaa 2850
 267 Glu Asn Phe Arg Thr Val Val Ser Leu Thr Gln Glu Gln Lys Phe Glu
 268 905 910 915
 270 cat atg tat gat cag agt ttg cag gta cca tac aga aac tct ttg agg 2898
 271 His Met Tyr Asp Gln Ser Leu Gln Val Pro Tyr Arg Asn Ser Leu Arg
 272 920 925 930
 274 aaa gca cac atc ttt gga atc acg ttt tcc ttc acg cag gca atg atg 2946
 275 Lys Ala His Ile Phe Gly Ile Thr Phe Ser Phe Thr Gln Ala Met Met
 276 935 940 945
 278 tat ttt tcc tat gct gga tgt ttc cgg ttt gga gcc tac ttg gtg gca 2994
 279 Tyr Phe Ser Tyr Ala Gly Cys Phe Arg Phe Gly Ala Tyr Leu Val Ala
 280 950 955 960 965
 282 cat agt ctc atg agc ttt gag gat gtt ctg tta gta ttt tca gct gtt 3042
 283 His Ser Leu Met Ser Phe Glu Asp Val Leu Leu Val Phe Ser Ala Val
 284 970 975 980
 286 gtc ttt ggt gcc atg gcc gtg ggg caa gtc agt tca ttt gct cct gac 3090
 287 Val Phe Gly Ala Met Ala Val Gly Gln Val Ser Ser Phe Ala Pro Asp
 288 985 990 995
 290 tat gcc aaa gcc aaa gta tca gca gcc cac atc atc atg atc att gaa 3138
 291 Tyr Ala Lys Ala Lys Val Ser Ala Ala His Ile Ile Met Ile Ile Glu
 292 1000 1005 1010
 294 aaa acc cct ttg att gac agc tac agc aca gaa ggc cta aag ccg aac 3186
 295 Lys Thr Pro Leu Ile Asp Ser Tyr Ser Thr Glu Gly Leu Lys Pro Asn
 296 1015 1020 1025
 298 aca ttg gaa gga aat gtc aca ttt aat gaa gtt gta ttc aac tat ccc 3234
 299 Thr Leu Glu Gly Asn Val Thr Phe Asn Glu Val Val Phe Asn Tyr Pro
 W--> 300 030 1030 1035 1040 1045
 302 acc cga ctg gac atc cca gtg ctt cag ggg ctg agc ctg gaa gtg aag 3282
 303 Thr Arg Leu Asp Ile Pro Val Leu Gln Gly Leu Ser Leu Glu Val Lys
 304 1050 1055 1060
 306 aag ggc cag acg ctg gcc ctg gtg ggc agc agt ggc tgt ggg aag agc 3330
 307 Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser Gly Cys Gly Lys Ser
 308 1065 1070 1075
 310 acg gtg gtc cag ctc ctg gag cgg ttc tat gac ccc ttg gcg ggg aaa 3378
 311 Thr Val Val Gln Leu Leu Glu Arg Phe Tyr Asp Pro Leu Ala Gly Lys
 312 1080 1085 1090
 314 gtg ctg ctt gac ggc aaa gaa ata aag caa ctg aat gtt cag tgg ctc 3426
 315 Val Leu Leu Asp Gly Lys Glu Ile Lys Gln Leu Asn Val Gln Trp Leu
 316 1095 1100 1105
 318 cga gca cac ctg ggc atc gtg tcc cag gag ccc atc ctg ttt gac tgc 3474

When
 numbering
 the first
 amino acid
 on a line,
 begin the
 number
 directly
 under the
 first letter
 of the amino
 acid

e.g. Thr | 1030 | Leu
 | 1031 |
 | 1032 |

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Input Set : A:\G00307-70020.txt

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323 Ser Ile Ser Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg Val Val Ser
324 1130 1135 1140
326 cag gaa gag atc gtg agg gca gcc aag gag gcc aat ata cac gcc ttc 3570
327 Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala Asn Ile His Ala Phe
328 1145 1150 1155
330 atc gag tca ctg cct aat aaa tat agc acc aga gta gga gac aaa gga 3618
331 Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Arg Val Gly Asp Lys Gly
332 1160 1165 1170
334 act cag ctc tct ggt ggc cag aaa caa cgc att gcc ata gct cgt gcc 3666
335 Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile Ala Arg Ala
336 1175 1180 1185
338 ctt gtt aga cag cct cat att ttg ctt ttg gat gaa gcc aca tca gct 3714
339 Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp Glu Ala Thr Ser Ala
W--> 340 190 1190 1195 1200 1205
342 ctg gat aca gaa agt gaa aag gtt gtc caa gaa gcc ctg gac aaa gcc 3762
343 Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu Ala Leu Asp Lys Ala
344 1210 1215 1220
346 aga gaa ggc cgt acc tgc att gtg att gct cac cgc ctg tcc acc atc 3810
347 Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His Arg Leu Ser Thr Ile
348 1225 1230 1235
350 cag aat gca gac tta ata gtg gtg ttt cag aat ggc aga gtc aag gag 3858
351 Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly Arg Val Lys Glu
352 1240 1245 1250
354 cac ggc aca cat cag cag ctg ctg gca cag aaa ggc atc tat ttt tca 3906
355 His Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile Tyr Phe Ser
356 1255 1260 1265
358 atg gtc agt gtc cag gct gga gca aag cgc cag t gaactgtgac 3950
359 Met Val Ser Val Gln Ala Gly Ala Lys Arg Gln
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362 tgtatgagat gttaaatatt ttttaaatatt tgtgttttaa tatggcattt attcaaagtt 4010
363 aaaaagcaag tacttataga attatgaaga gttatctgtt taacatttcc tcaaccaagt 4070
364 tcagagtctt cagacactcg taattaaagg aagagagcga gagacatcat caagtggaga 4130
E--> 365 gaaataatgg tttaaattgc attataaatt ttataacaga gttaaagtag attttt 4186-Insert
534 <210> SEQ ID NO: 3
535 <211> LENGTH: 4195
536 <212> TYPE: DNA
537 <213> ORGANISM: Macaca fascicularis
539 <220> FEATURE:
540 <221> NAME/KEY: CDS
541 <222> LOCATION: (100)...(3949)
543 <400> SEQUENCE: 3
544 gccgctggtt cgtttccgct aggtctttcc actaaagtcg gagtatcttc ttccaaaatt 60
545 tcacgacttg gtggccgttc caaggagcgc gaggtcggg atg gat ctt gaa ggg 114
546 Met Asp Leu Glu Gly
547 1 5
549 gac cgc aat gga gga gca gag aag aag aac ttt ttt aaa ctg aac aat 162

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550	Asp	Arg	Asn	Gly	Gly	Ala	Glu	Lys	Lys	Asn	Phe	Phe	Lys	Leu	Asn	Asn	
551					10					15					20		
553	aaa	agt	aaa	aaa	gat	aag	aag	gaa	agg	aaa	cca	act	gtc	agt	gta	ttt	210
554	Lys	Ser	Lys	Lys	Asp	Lys	Lys	Glu	Arg	Lys	Pro	Thr	Val	Ser	Val	Phe	
555				25					30					35			
557	tca	atg	ttt	cgc	tat	tca	aat	tgg	ctt	gac	aag	ttg	tat	atg	gtg	gtg	258
558	Ser	Met	Phe	Arg	Tyr	Ser	Asn	Trp	Leu	Asp	Lys	Leu	Tyr	Met	Val	Val	
559			40					45					50				
561	gga	act	ttg	gct	gcc	atc	atc	cat	gga	gct	gga	ctt	cct	ctc	atg	atg	306
562	Gly	Thr	Leu	Ala	Ala	Ile	Ile	His	Gly	Ala	Gly	Leu	Pro	Leu	Met	Met	
563		55					60					65					
565	ctg	gtg	ttt	gga	gac	atg	acg	gat	acc	ttt	gca	aat	gca	gga	aat	tta	354
566	Leu	Val	Phe	Gly	Asp	Met	Thr	Asp	Thr	Phe	Ala	Asn	Ala	Gly	Asn	Leu	
567	70					75					80					85	
569	gga	gat	tta	gga	gct	ctg	ttg	ttt	aac	aac	act	aat	agc	agt	aat	atc	402
570	Gly	Asp	Leu	Gly	Ala	Leu	Leu	Phe	Asn	Asn	Thr	Asn	Ser	Ser	Asn	Ile	
571					90					95					100		
573	act	gat	aca	gtg	ccc	gtc	atg	aat	ctg	gag	gaa	gat	atg	acc	agg	tat	450
574	Thr	Asp	Thr	Val	Pro	Val	Met	Asn	Leu	Glu	Glu	Asp	Met	Thr	Arg	Tyr	
575				105					110					115			
577	gcc	tat	tat	tac	agt	gga	att	ggg	gct	ggg	gtg	ctg	gtt	gct	gct	tac	498
578	Ala	Tyr	Tyr	Tyr	Ser	Gly	Ile	Gly	Ala	Gly	Val	Leu	Val	Ala	Ala	Tyr	
579			120					125					130				
581	att	cag	gtt	tca	ttt	tgg	tgc	ctg	gca	gct	gga	aga	caa	ata	cac	aaa	546
582	Ile	Gln	Val	Ser	Phe	Trp	Cys	Leu	Ala	Ala	Gly	Arg	Gln	Ile	His	Lys	
583		135					140					145					
585	att	aga	aaa	cag	ttt	ttt	cat	gct	ata	atg	cga	cag	gag	ata	ggc	tgg	594
586	Ile	Arg	Lys	Gln	Phe	Phe	His	Ala	Ile	Met	Arg	Gln	Glu	Ile	Gly	Trp	
587	150					155					160					165	
589	ttt	gat	gtg	cac	gat	gtt	ggg	gag	ctt	aac	acc	cgg	ctt	aca	gat	gat	642
590	Phe	Asp	Val	His	Asp	Val	Gly	Glu	Leu	Asn	Thr	Arg	Leu	Thr	Asp	Asp	
591				170					175					180			
593	gtc	tcc	aag	att	aat	gaa	gga	att	ggg	gac	aaa	att	gga	atg	ttc	ttt	690
594	Val	Ser	Lys	Ile	Asn	Glu	Gly	Ile	Gly	Asp	Lys	Ile	Gly	Met	Phe	Phe	
595				185					190					195			
597	cag	tca	atg	gca	aca	ttt	ttc	act	ggg	ttt	ata	gta	gga	ttt	aca	cgt	738
598	Gln	Ser	Met	Ala	Thr	Phe	Phe	Thr	Gly	Phe	Ile	Val	Gly	Phe	Thr	Arg	
599			200					205					210				
601	ggg	tgg	aag	cta	acc	ctt	gtg	att	ttg	gcc	atc	agt	cct	gtt	ctt	gga	786
602	Gly	Trp	Lys	Leu	Thr	Leu	Val	Ile	Leu	Ala	Ile	Ser	Pro	Val	Leu	Gly	
603		215					220					225					
605	ctg	tca	gct	gca	gtc	tgg	gca	aag	ata	ctg	tct	tca	ttt	act	gat	aaa	834
606	Leu	Ser	Ala	Ala	Val	Trp	Ala	Lys	Ile	Leu	Ser	Ser	Phe	Thr	Asp	Lys	
607	230					235				240					245		
609	gaa	ctc	tta	gct	tat	gca	aaa	gct	gga	gca	gta	gct	gaa	gag	gtc	ttg	882
610	Glu	Leu	Leu	Ala	Tyr	Ala	Lys	Ala	Gly	Ala	Val	Ala	Glu	Glu	Val	Leu	
611				250					255					260			
613	gca	gca	att	aga	act	gtg	att	gca	ttt	gga	gga	caa	aag	aaa	gaa	ctc	930
614	Ala	Ala	Ile	Arg	Thr	Val	Ile	Ala	Phe	Gly	Gly	Gln	Lys	Lys	Glu	Leu	

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615		265		270		275		
617	gaa agg tac aac aaa aat tta gaa gaa gct aaa aga att ggg ata aag							978
618	Glu Arg Tyr Asn Lys Asn Leu Glu Glu Ala Lys Arg Ile Gly Ile Lys							
619		280		285		290		
621	aaa gct att aca gcc aat att tct ata ggt gct gct ttc ctg ctt atc							1026
622	Lys Ala Ile Thr Ala Asn Ile Ser Ile Gly Ala Ala Phe Leu Leu Ile							
623		295		300		305		
625	tat gca tct tat gct ctg gcc ttc tgg tat ggg acc acc ttg gtc ctc							1074
626	Tyr Ala Ser Tyr Ala Leu Ala Phe Trp Tyr Gly Thr Thr Leu Val Leu							
627		310		315		320		325
629	tca aag gaa tat tct att gga caa gta ctc act gta ttc ttt tct gta							1122
630	Ser Lys Glu Tyr Ser Ile Gly Gln Val Leu Thr Val Phe Phe Ser Val							
631		330		335		340		
633	tta att ggg gct ttt agt gtt gga cag gca tct cca agc att gaa gca							1170
634	Leu Ile Gly Ala Phe Ser Val Gly Gln Ala Ser Pro Ser Ile Glu Ala							
635		345		350		355		
637	ttt gca aat gca aga gga gca gct ttt gaa atc ttc aag ata att gat							1218
638	Phe Ala Asn Ala Arg Gly Ala Ala Phe Glu Ile Phe Lys Ile Ile Asp							
639		360		365		370		
641	aat aag cca agt att gac agc tat tcg aag agt ggg cac aaa cca gat							1266
642	Asn Lys Pro Ser Ile Asp Ser Tyr Ser Lys Ser Gly His Lys Pro Asp							
643		375		380		385		
645	aat att aag gga aat ttg gaa ttc aga aat gtt cac ttc agt tac cca							1314
646	Asn Ile Lys Gly Asn Leu Glu Phe Arg Asn Val His Phe Ser Tyr Pro							
647		390		395		400		405
649	tct cga aaa gaa gtt aag atc ttg aag ggc ctg aac ctg aag gtg cag							1362
650	Ser Arg Lys Glu Val Lys Ile Leu Lys Gly Leu Asn Leu Lys Val Gln							
651		410		415		420		
653	agt ggg cag acg gtg gcc ctg gtt gga aac agc ggc tgt ggg aag agc							1410
654	Ser Gly Gln Thr Val Ala Leu Val Gly Asn Ser Gly Cys Gly Lys Ser							
655		425		430		435		
657	aca acg gtc cag ctg atg cag agg ctt tat gac ccc aca gag ggc atg							1458
658	Thr Thr Val Gln Leu Met Gln Arg Leu Tyr Asp Pro Thr Glu Gly Met							
659		440		445		450		
661	gtc agt gtt gat gga cag gat att agg acc ata aac gta agg ttt cta							1506
662	Val Ser Val Asp Gly Gln Asp Ile Arg Thr Ile Asn Val Arg Phe Leu							
663		455		460		465		
665	cgg gaa atc atc ggt gtg gtg agt cag gaa cct gta ttg ttt gcc acc							1554
666	Arg Glu Ile Ile Gly Val Val Ser Gln Glu Pro Val Leu Phe Ala Thr							
667		470		475		480		485
669	acg ata gct gaa aac att cgc tat ggt cgt gaa gat gtc acc atg gat							1602
670	Thr Ile Ala Glu Asn Ile Arg Tyr Gly Arg Glu Asp Val Thr Met Asp							
671		490		495		500		
673	gag att gag aaa gct gtc aag gaa gcc aat gcc tat gac ttt atc atg							1650
674	Glu Ile Glu Lys Ala Val Lys Glu Ala Asn Ala Tyr Asp Phe Ile Met							
675		505		510		515		
677	aaa ctg cct cag aaa ttt gac acc ctg gtt gga gag aga ggg gcc cag							1698
678	Lys Leu Pro Gln Lys Phe Asp Thr Leu Val Gly Glu Arg Gly Ala Gln							
679		520		525		530		

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681	ctg	agt	ggt	ggg	cag	aag	cag	agg	atc	gcc	att	gca	cgt	gcc	ctg	gtt	1746
682	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Leu	Val	
683		535					540					545					
685	cgc	aac	ccc	aag	atc	ctc	ctg	ctg	gac	gag	gcc	acg	tca	gcc	ttg	gac	1794
686	Arg	Asn	Pro	Lys	Ile	Leu	Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp		
687	550					555				560					565		
689	aca	gaa	agt	gaa	gca	gtg	gtt	cag	gtg	gct	ctg	gat	aag	gcc	aga	aaa	1842
690	Thr	Glu	Ser	Glu	Ala	Val	Val	Gln	Val	Ala	Leu	Asp	Lys	Ala	Arg	Lys	
691					570					575					580		
693	ggt	cgg	acc	acc	att	gtg	ata	gct	cat	cgt	ttg	tct	acg	gtt	cgt	aat	1890
694	Gly	Arg	Thr	Thr	Ile	Val	Ile	Ala	His	Arg	Leu	Ser	Thr	Val	Arg	Asn	
695					585				590					595			
697	gcc	gac	gtc	atc	gct	ggt	ttc	gat	gat	gga	gtc	att	gtg	gag	aaa	gga	1938
698	Ala	Asp	Val	Ile	Ala	Gly	Phe	Asp	Asp	Gly	Val	Ile	Val	Glu	Lys	Gly	
699			600					605					610				
701	aat	cat	gat	gag	ctc	atg	aaa	gag	aaa	ggc	att	tac	ttc	aaa	ctt	gtc	1986
702	Asn	His	Asp	Glu	Leu	Met	Lys	Glu	Lys	Gly	Ile	Tyr	Phe	Lys	Leu	Val	
703			615				620					625					
705	aca	atg	cag	aca	gca	gga	aat	gaa	att	gaa	tta	gaa	aat	gca	gct	gat	2034
706	Thr	Met	Gln	Thr	Ala	Gly	Asn	Glu	Ile	Glu	Leu	Glu	Asn	Ala	Ala	Asp	
707	630					635					640					645	
709	gaa	tcc	aaa	agt	gaa	att	gat	acc	ttg	gaa	atg	tct	tca	cat	gat	tca	2082
710	Glu	Ser	Lys	Ser	Glu	Ile	Asp	Thr	Leu	Glu	Met	Ser	Ser	His	Asp	Ser	
711					650					655					660		
713	gga	tcc	agt	cta	ata	aga	aaa	aga	tcc	act	cgt	agg	agt	gtc	cgt	gga	2130
714	Gly	Ser	Ser	Leu	Ile	Arg	Lys	Arg	Ser	Thr	Arg	Arg	Ser	Val	Arg	Gly	
715					665				670					675			
717	tca	caa	ggc	caa	gac	aga	aag	ctt	agt	acc	aaa	gag	gct	ctg	gat	gaa	2178
718	Ser	Gln	Gly	Gln	Asp	Arg	Lys	Leu	Ser	Thr	Lys	Glu	Ala	Leu	Asp	Glu	
719			680					685				690					
721	agt	ata	cct	cca	gtt	tcc	ttt	tgg	agg	att	atg	aag	cta	aat	tta	act	2226
722	Ser	Ile	Pro	Pro	Val	Ser	Phe	Trp	Arg	Ile	Met	Lys	Leu	Asn	Leu	Thr	
723			695				700					705					
725	gag	tgg	cct	tat	ttt	gtt	gtt	ggt	gta	ttt	tgt	gcc	att	ata	aat	gga	2274
726	Glu	Trp	Pro	Tyr	Phe	Val	Val	Gly	Val	Phe	Cys	Ala	Ile	Ile	Asn	Gly	
727	710					715					720				725		
729	ggt	ctg	caa	cca	gca	ttt	gca	gta	ata	ttt	tca	aag	att	ata	ggg	att	2322
730	Gly	Leu	Gln	Pro	Ala	Phe	Ala	Val	Ile	Phe	Ser	Lys	Ile	Ile	Gly	Ile	
731					730					735					740		
733	ttt	aca	aga	aat	gat	gat	gcc	gaa	aca	aaa	cga	cag	aat	agt	aac	ttg	2370
734	Phe	Thr	Arg	Asn	Asp	Asp	Ala	Glu	Thr	Lys	Arg	Gln	Asn	Ser	Asn	Leu	
735					745				750					755			
737	ttt	tca	cta	ttg	ttt	cta	gtc	ctt	gga	att	gtt	tct	ttt	att	aca	ttt	2418
738	Phe	Ser	Leu	Leu	Phe	Leu	Val	Leu	Gly	Ile	Val	Ser	Phe	Ile	Thr	Phe	
739			760					765					770				
741	ttc	ctt	cag	ggc	ttc	aca	ttt	ggc	aaa	gct	gga	gag	atc	ctc	acc	aag	2466
742	Phe	Leu	Gln	Gly	Phe	Thr	Phe	Gly	Lys	Ala	Gly	Glu	Ile	Leu	Thr	Lys	
743			775				780					785					
745	cgg	ctc	cga	tac	atg	gtt	ttc	cga	tcc	atg	ctc	aga	cag	gat	gtg	agc	2514

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746	Arg	Leu	Arg	Tyr	Met	Val	Phe	Arg	Ser	Met	Leu	Arg	Gln	Asp	Val	Ser	
747	790					795					800					805	
749	tgg	ttt	gat	gac	cct	aaa	aac	acc	act	gga	gca	ttg	act	acc	agg	ctc	2562
750	Trp	Phe	Asp	Asp	Pro	Lys	Asn	Thr	Thr	Gly	Ala	Leu	Thr	Thr	Arg	Leu	
751					810					815					820		
753	gcc	aat	gat	gct	gct	caa	gtt	aaa	ggg	gct	ata	ggg	tcc	agg	ctt	gct	2610
754	Ala	Asn	Asp	Ala	Ala	Gln	Val	Lys	Gly	Ala	Ile	Gly	Ser	Arg	Leu	Ala	
755					825				830					835			
757	ata	att	acc	cag	aat	ata	gca	aat	ctt	ggg	aca	gga	ata	att	ata	tcc	2658
758	Ile	Ile	Thr	Gln	Asn	Ile	Ala	Asn	Leu	Gly	Thr	Gly	Ile	Ile	Ile	Ser	
759				840				845					850				
761	tta	atc	tat	ggg	tgg	caa	ctg	aca	ctg	tta	ctc	tta	gca	att	gta	ccc	2706
762	Leu	Ile	Tyr	Gly	Trp	Gln	Leu	Thr	Leu	Leu	Leu	Leu	Ala	Ile	Val	Pro	
763		855				860					865						
765	atc	att	gca	ata	gca	gga	gtt	gtt	gaa	atg	aaa	atg	ttg	tct	gga	caa	2754
766	Ile	Ile	Ala	Ile	Ala	Gly	Val	Val	Glu	Met	Lys	Met	Leu	Ser	Gly	Gln	
767	870				875				880						885		
769	gca	ctg	aaa	gat	aag	aaa	gaa	cta	gaa	ggg	gct	ggg	aag	atc	gct	act	2802
770	Ala	Leu	Lys	Asp	Lys	Lys	Glu	Leu	Glu	Gly	Ala	Gly	Lys	Ile	Ala	Thr	
771				890					895					900			
773	gaa	gca	ata	gaa	aac	ttc	cga	act	gtt	gtt	tct	ttg	act	cag	gag	cag	2850
774	Glu	Ala	Ile	Glu	Asn	Phe	Arg	Thr	Val	Val	Ser	Leu	Thr	Gln	Glu	Gln	
775				905					910					915			
777	aag	ttt	gaa	cat	atg	tat	gat	cag	agt	ttg	cag	gta	cca	tac	aga	aac	2898
778	Lys	Phe	Glu	His	Met	Tyr	Asp	Gln	Ser	Leu	Gln	Val	Pro	Tyr	Arg	Asn	
779			920				925						930				
781	tct	ttg	agg	aaa	gca	cac	atc	ttt	gga	atc	acg	ttt	tcc	ttc	acg	cag	2946
782	Ser	Leu	Arg	Lys	Ala	His	Ile	Phe	Gly	Ile	Thr	Phe	Ser	Phe	Thr	Gln	
783		935				940					945						
785	gca	atg	atg	tat	ttt	tcc	tat	gct	gga	tgt	ttc	cgg	ttt	gga	gcc	tac	2994
786	Ala	Met	Met	Tyr	Phe	Ser	Tyr	Ala	Gly	Cys	Phe	Arg	Phe	Gly	Ala	Tyr	
787	950				955				960					965			
789	ttg	gtg	gca	cat	agt	ctc	atg	agc	ttt	gag	gat	gtt	ctg	tta	gta	ttt	3042
790	Leu	Val	Ala	His	Ser	Leu	Met	Ser	Phe	Glu	Asp	Val	Leu	Leu	Val	Phe	
791				970					975					980			
793	tca	gct	gtt	gtc	ttt	ggg	gcc	atg	gcc	gtg	ggg	caa	gtc	agt	tca	ttt	3090
794	Ser	Ala	Val	Val	Phe	Gly	Ala	Met	Ala	Val	Gly	Gln	Val	Ser	Ser	Phe	
795				985					990					995			
797	gct	cct	gac	tat	gcc	aaa	gcc	aaa	gta	tca	gca	gcc	cac	atc	atc	atg	3138
798	Ala	Pro	Asp	Tyr	Ala	Lys	Ala	Lys	Val	Ser	Ala	Ala	His	Ile	Ile	Met	
799		1000					1005					1010					
801	atc	att	gaa	aaa	acc	cct	ttg	att	gac	agc	tac	agc	aca	gaa	ggc	cta	3186
802	Ile	Ile	Glu	Lys	Thr	Pro	Leu	Ile	Asp	Ser	Tyr	Ser	Thr	Glu	Gly	Leu	
803		1015				1020					1025						
805	aag	ccg	aac	aca	ttg	gaa	gga	aat	gtc	aca	ttt	aat	gaa	gtt	gta	ttc	3234
806	Lys	Pro	Asn	Thr	Leu	Glu	Gly	Asn	Val	Thr	Phe	Asn	Glu	Val	Val	Phe	
W--> 807	030	1030			1035				1040					1045			
809	aac	tat	ccc	acc	cga	ctg	gac	atc	cca	gtg	ctt	cag	ggg	ctg	agc	ctg	3282
810	Asn	Tyr	Pro	Thr	Arg	Leu	Asp	Ile	Pro	Val	Leu	Gln	Gly	Leu	Ser	Leu	

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811          1050          1055          1060
813 gaa gtg aag aag ggc cag acg ctg gcc ctg gtg ggc agc agt ggc tgt 3330
814 Glu Val Lys Lys Gly Gln Thr Leu Ala Leu Val Gly Ser Ser Gly Cys
815          1065          1070          1075
817 ggg aag agc acg gtg gtc cag ctc ctg gag cgg ttc tat gac ccc ttg 3378
818 Gly Lys Ser Thr Val Val Gln Leu Glu Arg Phe Tyr Asp Pro Leu
819          1080          1085          1090
821 gcg ggg aaa gtg ctg ctt gac ggc aaa gaa ata aag caa ctg aat gtt 3426
822 Ala Gly Lys Val Leu Leu Asp Gly Lys Glu Ile Lys Gln Leu Asn Val
823          1095          1100          1105
825 cag tgg ctc cga gca cac ctg ggc atc gtg tcc cag gag ccc atc ctg 3474
826 Gln Trp Leu Arg Ala His Leu Gly Ile Val Ser Gln Glu Pro Ile Leu
W--> 827 110 ///0          1115          1120          1125
829 ttt gac tgc agc att agt gag aac att gcc tat gga gac aac agc cgg 3522
830 Phe Asp Cys Ser Ile Ser Glu Asn Ile Ala Tyr Gly Asp Asn Ser Arg
831          1130          1135          1140
833 gtg gtg tca cag gaa gag atc gtg agg gca gcc aag gag gcc aat ata 3570
834 Val Val Ser Gln Glu Glu Ile Val Arg Ala Ala Lys Glu Ala Asn Ile
835          1145          1150          1155
837 cac gcc ttc atc gag tca ctg cct aat aaa tat agc acc aga gta gga 3618
838 His Ala Phe Ile Glu Ser Leu Pro Asn Lys Tyr Ser Thr Arg Val Gly
839          1160          1165          1170
841 gac aaa gga act cag ctc tct ggt ggc cag aaa caa cgc att gcc ata 3666
842 Asp Lys Gly Thr Gln Leu Ser Gly Gly Gln Lys Gln Arg Ile Ala Ile
843          1175          1180          1185
845 gct cgt gcc ctt gtt aga cag cct cat att ttg ctt ttg gat gaa gcc 3714
846 Ala Arg Ala Leu Val Arg Gln Pro His Ile Leu Leu Leu Asp Glu Ala
W--> 847 190 1190          1195          1200          1205
849 aca tca gct ctg gat aca gaa agt gaa aag gtt gtc caa gaa gcc ctg 3762
850 Thr Ser Ala Leu Asp Thr Glu Ser Glu Lys Val Val Gln Glu Ala Leu
851          1210          1215          1220
853 gac aaa gcc aga gaa ggc cgt acc tgc att gtg att gct cac cgc ctg 3810
854 Asp Lys Ala Arg Glu Gly Arg Thr Cys Ile Val Ile Ala His Arg Leu
855          1225          1230          1235
857 tcc acc atc cag aat gca gac tta ata gtg gtg ttt cag aat ggc aga 3858
858 Ser Thr Ile Gln Asn Ala Asp Leu Ile Val Val Phe Gln Asn Gly Arg
859          1240          1245          1250
861 gtc aag gag cac ggc aca cat cag cag ctg ctg gca cag aaa ggc atc 3906
862 Val Lys Glu His Gly Thr His Gln Gln Leu Leu Ala Gln Lys Gly Ile
863          1255          1260          1265
865 tat ttt tca atg gtc agt gtc cag gct gga gca aag cgc cag t 3949
866 Tyr Phe Ser Met Val Ser Val Gln Ala Gly Ala Lys Arg Gln
W--> 867 270 1270          1275          1280
869 gaactgtgac tgtatgagat gttaaattatt ttttaattatt tgtgttttaa tatggcattt 4009
870 attcaaagtt aaaaagcaag tacttataga attatgaaga gttatctgtt taacatttcc 4069
871 tcaaccaagt tcagagtctt cagacactcg taattaaagg aagagagcga gagacatcat 4129
872 caagtggaga gaaataatgg tttaaattgc attataaatt ttataacaga gttaaagtag 4189
E--> 873 atttttt

```

4195 ← insert

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/619,359

DATE: 07/28/2003

TIME: 08:59:08

Input Set : A:\G00307-70020.txt

Output Set: N:\CRF4\07282003\J619359.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:300 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:320 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:340 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:365 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:4186 SEQ:1
L:807 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:827 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:873 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:4195 SEQ:3